

#4



IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re Application of: :
Doetsch et al. : Group Art Unit: 1645
Serial No. 09/724,296 : Examiner: Not yet assigned
Filed: November 28, 2000
For: BROAD SPECIFICITY DNA DAMAGE ENDONUCLEASE

STATEMENT UNDER 37 C.F.R. §1.821-824

Assistant Commissioner for Patents
Box Missing Parts
Washington, D.C. 20231

Sir:

The above-identified patent application contains sequences as defined in 37 C.F.R. §1.821(a). Accordingly, the specification includes a paper copy of Sequence Listing as pages 1 - 36. Applicants also submit a write-protected diskette copy of the Sequence Listing in computer-readable form as required by 37 C.F.R. §1.821(e). All of the sequences now presented in the Sequence Listing are found in the as-filed application. Accordingly, the present Sequence Listing does not constitute the addition of new matter.

In compliance with 37 C.F.R. §1.821(f), the undersigned states that the content of the paper copies and computer-readable copies of the Sequence Listing are the same.

Respectfully submitted,

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Reg. No. 33,878

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Attorney Docket No.: 25-98A
bmk: May 17, 2001

CERTIFICATE OF MAILING	
I hereby certify that this correspondence is being deposited with the United States Postal Service with sufficient postage as first class mail in an envelope addressed to the Assistant Commissioner for Patents, Washington, D.C., 20231	
<u>17 May 2001</u> Date	<u>B. Kroge</u> B. Kroge

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#4



SEQUENCE LISTING

<110> Doetsch, Paul W.
Avery, Angela M.
Kaur, Balveen

<120> Broad Specificity DNA Damage Endonuclease

<130> 25-98A

<140> US/09/724,296

<141> 2000-11-28

<150> US/09/327,984

<151> 1999-06-08

<150> US/60/088,521

<151> 1998-06-08

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<151> 1999-05-18

<160> 71

<170> PatentIn Ver. 2.0

<210> 1

<211> 2492

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Coding
sequence for fusion protein of GST signal peptide
and the UVDE protein of Schizosaccharomyces pombe

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tattgatggg gatgttaaata taacacagtc tatggccatc atacgttata tagctgacaa 240
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gggaattaca cagaagcaac attactcaga atcggtgat ccaacggcga tttctgggat 2220
gaaacgacgt gctcactctg ataggtgtt tgactttcca ccgtgtgat ctacaatgga 2280
tctaataata gaagctaagg aaaaggaaca ggctgtattt gaattgtgta gacgttatga 2340
gttacaaaaa ccaccatgct ctcttgaaat tatggggcct gaatacgatc aaactcgaga 2400
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<212> PRT

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Fusion protein
of GST leader peptide and Schizosaccharomyces
pombe UVDE

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His Leu Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe
35 40 45

Glu Leu Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp
50 55 60

Val Lys Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys
 65 70 75 80
 His Asn Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met
 85 90 95
 Leu Glu Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala
 100 105 110
 Tyr Ser Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu
 115 120 125
 Pro Glu Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr
 130 135 140
 Leu Asn Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala
 145 150 155 160
 Leu Asp Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro
 165 170 175
 Lys Leu Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp
 180 185 190
 Lys Tyr Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp
 195 200 205
 Gln Ala Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp His Leu
 210 215 220
 Val Pro Arg Gly Ser Met Leu Arg Leu Leu Lys Arg Asn Ile Gln Ile
 225 230 235 240
 Ser Lys Arg Ile Val Phe Thr Ile Leu Lys Gln Lys Ala Phe Lys Gly
 245 250 255
 Asn His Pro Cys Val Pro Ser Val Cys Thr Ile Thr Tyr Ser Arg Phe
 260 265 270
 His Cys Leu Pro Asp Thr Leu Lys Ser Leu Leu Pro Met Ser Ser Lys
 275 280 285
 Thr Thr Leu Ser Met Leu Pro Gln Val Asn Ile Gly Ala Asn Ser Phe
 290 295 300
 Ser Ala Glu Thr Pro Val Asp Leu Lys Lys Glu Asn Glu Thr Glu Leu
 305 310 315 320
 Ala Asn Ile Ser Gly Pro His Lys Lys Ser Thr Ser Thr Ser Thr Arg
 325 330 335

Lys Arg Ala Arg Ser Ser Lys Lys Lys Ala Thr Asp Ser Val Ser Asp
 340 345 350
 Lys Ile Asp Glu Ser Val Ala Ser Tyr Asp Ser Ser Thr His Leu Arg
 355 360 365
 Arg Ser Ser Arg Ser Lys Lys Pro Val Asn Tyr Asn Ser Ser Ser Glu
 370 375 380
 Ser Glu Ser Glu Glu Gln Ile Ser Lys Ala Thr Lys Lys Val Lys Gln
 385 390 395 400
 Lys Glu Glu Glu Glu Tyr Val Glu Glu Val Asp Glu Lys Ser Leu Lys
 405 410 415
 Asn Glu Ser Ser Ser Asp Glu Phe Glu Pro Val Val Pro Glu Gln Leu
 420 425 430
 Glu Thr Pro Ile Ser Lys Arg Arg Arg Ser Arg Ser Ser Ala Lys Asn
 435 440 445
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 450 455 460
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 465 470 475 480
 Tyr Ala Cys Leu Asn Thr Ile Leu Arg Ser Met Lys Glu Arg Val Phe
 485 490 495
 Cys Ser Arg Thr Cys Arg Ile Thr Thr Ile Gln Arg Asp Gly Leu Glu
 500 505 510
 Ser Val Lys Gln Leu Gly Thr Gln Asn Val Leu Asp Leu Ile Lys Leu
 515 520 525
 Val Glu Trp Asn His Asn Phe Gly Ile His Phe Met Arg Val Ser Ser
 530 535 540
 Asp Leu Phe Pro Phe Ala Ser His Ala Lys Tyr Gly Tyr Thr Leu Glu
 545 550 555 560
 Phe Ala Gln Ser His Leu Glu Glu Val Gly Lys Leu Ala Asn Lys Tyr
 565 570 575
 Asn His Arg Leu Thr Met His Pro Gly Gln Tyr Thr Gln Ile Ala Ser
 580 585 590
 Pro Arg Glu Val Val Val Asp Ser Ala Ile Arg Asp Leu Ala Tyr His
 595 600 605

Asp Glu Ile Leu Ser Arg Met Lys Leu Asn Glu Gln Leu Asn Lys Asp
 610 615 620
 Ala Val Leu Ile Ile His Leu Gly Gly Thr Phe Glu Gly Lys Lys Glu
 625 630 635 640
 Thr Leu Asp Arg Phe Arg Lys Asn Tyr Gln Arg Leu Ser Asp Ser Val
 645 650 655
 Lys Ala Arg Leu Val Leu Glu Asn Asp Asp Val Ser Trp Ser Val Gln
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 Asp Leu Leu Pro Leu Cys Gln Glu Leu Asn Ile Pro Leu Val Leu Asp
 675 680 685
 Trp His His His Asn Ile Val Pro Gly Thr Leu Arg Glu Gly Ser Leu
 690 695 700
 Asp Leu Met Pro Leu Ile Pro Thr Ile Arg Glu Thr Trp Thr Arg Lys
 705 710 715 720
 Gly Ile Thr Gln Lys Gln His Tyr Ser Glu Ser Ala Asp Pro Thr Ala
 725 730 735
 Ile Ser Gly Met Lys Arg Arg Ala His Ser Asp Arg Val Phe Asp Phe
 740 745 750
 Pro Pro Cys Asp Pro Thr Met Asp Leu Met Ile Glu Ala Lys Glu Lys
 755 760 765
 Glu Gln Ala Val Phe Glu Leu Cys Arg Arg Tyr Glu Leu Gln Asn Pro
 770 775 780
 Pro Cys Pro Leu Glu Ile Met Gly Pro Glu Tyr Asp Gln Thr Arg Asp
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<210> 3
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 <213> Schizosaccharomyces pombe

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<223> DNA sequence encoding UVDE protein, truncated at amino acid residue 228.

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actcgagatg gatattatcc gcccgagct gaaaagcgtt taactgcaag aaaaaggcgt 1080
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<211> 371

<212> PRT

<213> Schizosaccharomyces pombe

<220>

<221> VARIANT

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<223> Truncated version of the UVDE protein.

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Ser Met Lys Glu Arg Val Phe Cys Ser Arg Thr Cys Arg Ile Thr Thr
      35              40              45

Ile Gln Arg Asp Gly Leu Glu Ser Val Lys Gln Leu Gly Thr Gln Asn
      50              55              60

Val Leu Asp Leu Ile Lys Leu Val Glu Trp Asn His Asn Phe Gly Ile
      65              70              75              80

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002250 062436 09724260

His	Phe	Met	Arg	Val	Ser	Ser	Asp	Leu	Phe	Pro	Phe	Ala	Ser	His	Ala	
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Lys	Tyr	Gly	Tyr	Thr	Leu	Glu	Phe	Ala	Gln	Ser	His	Leu	Glu	Glu	Val	
			100					105					110			
Gly	Lys	Leu	Ala	Asn	Lys	Tyr	Asn	His	Arg	Leu	Thr	Met	His	Pro	Gly	
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Arg	Tyr	Glu	Leu	Gln	Asn	Pro	Pro	Cys	Pro	Leu	Glu	Ile	Met	Gly	Pro	
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Asp Glu Lys
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 <213> Artificial Sequence

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 sequence encoding fusion protein of GST signal
 peptide and the truncated version of *S. pombe* UVDE
 protein.

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<210> 6
 <211> 600
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Fusion protein
 comprising the GST signal peptide and the
 truncated UVDE protein of *S. pombe*.

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 35 40 45
 Glu Leu Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp
 50 55 60
 Val Lys Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys
 65 70 75 80
 His Asn Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met
 85 90 95
 Leu Glu Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala
 100 105 110
 Tyr Ser Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu
 115 120 125
 Pro Glu Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr
 130 135 140
 Leu Asn Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala
 145 150 155 160
 Leu Asp Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro
 165 170 175
 Lys Leu Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp
 180 185 190
 Lys Tyr Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp
 195 200 205

Gln Ala Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp His Leu
 210 215 220
 Val Pro Arg Gly Ser Asp Asp His Ala Pro Arg Glu Met Phe Asp Cys
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 Leu Asp Lys Pro Ile Pro Trp Arg Gly Arg Leu Gly Tyr Ala Cys Leu
 245 250 255
 Asn Thr Ile Leu Arg Ser Met Lys Glu Arg Val Phe Cys Ser Arg Thr
 260 265 270
 Cys Arg Ile Thr Thr Ile Gln Arg Asp Gly Leu Glu Ser Val Lys Gln
 275 280 285
 Leu Gly Thr Gln Asn Val Leu Asp Leu Ile Lys Leu Val Glu Trp Asn
 290 295 300
 His Asn Phe Gly Ile His Phe Met Arg Val Ser Ser Asp Leu Phe Pro
 305 310 315 320
 Phe Ala Ser His Ala Lys Tyr Gly Tyr Thr Leu Glu Phe Ala Gln Ser
 325 330 335
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 Thr Met His Pro Gly Gln Tyr Thr Gln Ile Ala Ser Pro Arg Glu Val
 355 360 365
 Val Val Asp Ser Ala Ile Arg Asp Leu Ala Tyr His Asp Glu Ile Leu
 370 375 380
 Ser Arg Met Lys Leu Asn Glu Gln Leu Asn Lys Asp Ala Val Leu Ile
 385 390 395 400
 Ile His Leu Gly Gly Thr Phe Glu Gly Lys Lys Glu Thr Leu Asp Arg
 405 410 415
 Phe Arg Lys Asn Tyr Gln Arg Leu Ser Asp Ser Val Lys Ala Arg Leu
 420 425 430
 Val Leu Glu Asn Asp Asp Val Ser Trp Ser Val Gln Asp Leu Leu Pro
 435 440 445
 Leu Cys Gln Glu Leu Asn Ile Pro Leu Val Leu Asp Trp His His His
 450 455 460
 Asn Ile Val Pro Gly Thr Leu Arg Glu Gly Ser Leu Asp Leu Met Pro
 465 470 475 480

Leu Ile Pro Thr Ile Arg Glu Thr Trp Thr Arg Lys Gly Ile Thr Gln
485 490 495

Lys Gln His Tyr Ser Glu Ser Ala Asp Pro Thr Ala Ile Ser Gly Met
500 505 510

Lys Arg Arg Ala His Ser Asp Arg Val Phe Asp Phe Pro Pro Cys Asp
515 520 525

Pro Thr Met Asp Leu Met Ile Glu Ala Lys Glu Lys Glu Gln Ala Val
530 535 540

Phe Glu Leu Cys Arg Arg Tyr Glu Leu Gln Asn Pro Pro Cys Pro Leu
545 550 555 560

Glu Ile Met Gly Pro Glu Tyr Asp Gln Thr Arg Asp Gly Tyr Tyr Pro
565 570 575

Pro Gly Ala Glu Lys Arg Leu Thr Ala Arg Lys Arg Arg Ser Arg Lys
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Glu Glu Val Glu Glu Asp Glu Lys
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<210> 7

<211> 688

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Nucleotide
sequence encoding GST signal peptide.

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gcacaacatg ttggttgggt gtccaaaaga gcgtgcagag atttcaatgc ttgaaggagc 300
ggttttggat attagatacg gtgtttcgag aattgcatat agtaaagact ttgaaactct 360
caaagttgat tttcttagca agctacctga aatgctgaaa atgttcgaag atcgtttatg 420
tcataaaaaca tatttaaata ttgaccatgt aacctatcct gacttcatgt tgtatgacgc 480
tcttgatggt gttttataca tggacccaat gtgcctggat gcgttcccaa aattagtttg 540
ttttaaaaaa cgtattgaag ctatcccaca aattgataag tacttgaaat ccagcaagta 600
tatagcatgg cctttgcagg gctggcaagc cacgtttggt ggtggcgacc atoctccaaa 660
atcgatcat ctggttccgc gtggatcc 688

<210> 8

<211> 229

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Amino acid
sequence of GST signal peptide

<400> 8

Met Thr Lys Leu Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val
1 5 10 15

Gln Pro Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu
20 25 30

His Leu Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe
35 40 45

Glu Leu Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp
50 55 60

Val Lys Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys
65 70 75 80

His Asn Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met
85 90 95

Leu Glu Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala
100 105 110

Tyr Ser Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu
115 120 125

Pro Glu Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr
130 135 140

Leu Asn Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala
145 150 155 160

Leu Asp Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro
165 170 175

Lys Leu Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp
180 185 190

Lys Tyr Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp
195 200 205

Gln Ala Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp His Leu
210 215 220

Val Pro Arg Gly Ser
225

<210> 9
 <211> 36
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:
 Oligonucleotide

<400> 9
 tgaggatcca atcgttttca ttttttaatg cttagg 36

<210> 10
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:
 Oligonucleotide

<400> 10
 ggccatgggtt atttttcac ctc 23

<210> 11
 <211> 28
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:
 Oligonucleotide

<400> 11
 aatgggatcc gatgatcatg ctccacga 28

<210> 12
 <211> 28
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:
 Oligonucleotide

<400> 12
 gggatcctta tttttcatcc tcttctac 28

<210> 13
 <211> 30

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Double
stranded oligonucleotide containing cis-syn
cyclobutane pyrimidine dimer.

<220>
<221> misc_feature
<222> (15)..(16)
<223> At positions 15- 16, the T-T is in the form of
cis-syn cyclobutane pyrimidine dimer.

<400> 13
catgcctgca cgaattaagc aattcgtaat 30

<210> 14
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Undamaged
double stranded oligonucleotide.

<400> 14
catgcctgca cgaattaagc aattcgtaat 30

<210> 15
<211> 49
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Double
stranded oligonucleotide containing cis-syn
cyclobutane dimer at positions 21-22.

<400> 15
agctaccatg cctgcacgaa ttaagcaatt cgtaatcatg gtcatagct 49

<210> 16
<211> 49
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Double
stranded oligonucleotide containing cis-syn
cyclobutane pyrimidine dimer at positions 21-22.

<400> 16
agctaccatg cctgcacgaa ttaagcaatt cgtaatcatg gtcatagct 49

<210> 17
<211> 49
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Double
stranded oligonucleotide containing trans- syn 11
cyclobutane pyrimidine dimer at positions 21-22.

<400> 17
agctaccatg cctgcacgaa ttaagcaatt cgtaatcatg gtcatagct 49

<210> 18
<211> 49
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Double
stranded oligonucleotide containing a 6-4 photo
product at position 21-22.

<400> 18
agctaccatg cctgcacgaa ttaagcaatt cgtaatcatg gtcatagct 49

<210> 19
<211> 49
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Double
stranded oligonucleotide containing a Dewar
isomer.

<400> 19
agctaccatg cctgcacgaa ttaagcaatt cgtaatcatg gtcatagct 49

<210> 20
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Double
stranded oligonucleotide containing cisplatin DNA
diadduct at position 16-17.

<400> 20
 tccctccttc cttccggccc tccttccct tc 32

<210> 21
 <211> 37
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Double
 stranded oligonucleotide wherein n is uracil at
 position 21.

<220>
 <221> misc_feature
 <222> (21)
 <223> The n at position 21 is uracil.

<400> 21
 cttggactgg atgtcggcac nagcggatac aggagca 37

<210> 22
 <211> 37
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Double
 stranded oligonucleotide wherein n is
 dihydrouracil at position 21.

<220>
 <221> misc_feature
 <222> (21)
 <223> At position 21, n is dihydrouracil.

<400> 22
 cttggactgg atgtcggcac nagcggatac aggagca 37

<210> 23
 <211> 37
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Double
 stranded oligonucleotide wherein n at position 21
 represents an abasic site.

<220>
 <221> misc_feature

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<222> (21)
 <223> At position 21, n is an abasic site.

 <400> 23
 cttggactgg atgtcggcac nagcggatac aggagca 37

 <210> 24
 <211> 31
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Double
 stranded oligonucleotide wherein n at position 13
 is an inosine.

 <220>
 <221> misc_feature
 <222> (13)
 <223> At position 13, n is inosine.

 <400> 24
 tgcaggtcga ctnaggagga tccccgggta c 31

 <210> 25
 <211> 31
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Double
 stranded oligonucleotide wherein n at position 13
 is xanthine.

 <220>
 <221> misc_feature
 <222> (13)
 <223> N at position 13 is xanthine.

 <400> 25
 tgcaggtcga ctnaggagga tccccgggta c 31

 <210> 26
 <211> 37
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Double
 stranded oligonucleotide wherein n at position 21
 is 8-oxoguanine.

<220>
 <221> misc_feature
 <222> (21)
 <223> N at position 21 is 8-oxoguanine.

 <400> 26
 cttggactgg atgtcggcac nagcggatac aggagca 37

 <210> 27
 <211> 30
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Double
 stranded oligonucleotide representing all 16
 possible base pair mismatches at position 18 in
 individual preparations.

 <220>
 <221> misc_feature
 <222> (18)
 <223> N at position 18 represents all 16 possible base
 pair mismatches.

 <400> 27
 gtacccgggg atcctccnag tcgacctgca 30

 <210> 28
 <211> 41
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Double
 stranded oligonucleotide containing a CA
 mismatched base pair at position 21.

 <220>
 <221> misc_feature
 <222> (21)
 <223> N at position 21 represents C of C/A mismatched
 base pair.

 <400> 28
 cgttagcatg cctgcacgaa ntaagcaatt cgtaatgcat t 41

 <210> 29
 <211> 41
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Double
 stranded oligonucleotide wherein there is a C/A
 mismatched base pair at position 36.

<220>
 <221> misc_feature
 <222> (36)
 <223> N at position 36 represents a C/A mismatched base
 pair.

<400> 29
 cggtacaagt ccgtcacgaa ttaagcaatt cgtaangcat t

41

<210> 30
 <211> 41
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Double
 stranded oligonucleotide wherein n at position 31
 represents a C/A mismatched base pair.

<220>
 <221> misc_feature
 <222> (31)
 <223> The n at position 31 represents C of C/A
 mismatched base pair.

<400> 30
 cggtacaagt ccgtcacgaa ttaagcaatt ngtaacgcat t

41

<210> 31
 <211> 41
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Double
 stranded oligonucleotide wherein n at position 26
 is a C/A mismatched base pair.

<220>
 <221> misc_feature
 <222> (26)
 <223> N at position 26 represents a C/A mismatched base
 pair.

<400> 31
 cggtacaagt ccgtcacgaa ttaagnaatt cgtaacgcat t

41

<210> 32
 <211> 41
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Description of Artificial Sequence: Double
 stranded oligonucleotide wherein n at position 21
 is a C/A mismatched base pair.

<220>
 <221> misc_feature
 <222> (21)
 <223> The n at position 21 represents a C/A mismatched
 base pair.

<400> 32
 cggtacaagt ccgtcacgac ntaagcaatt cgtaacgcat t

41

<210> 33
 <211> 41
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Double
 stranded oligonucleotide wherein n at position 15
 represents a C/A mismatched base pair.

<220>
 <221> misc_feature
 <222> (15)
 <223> The n at position 15 represents a C/A mismatched
 base pair.

<400> 33
 cggtacaagt ccgtnacgaa ttaagcaatt cgtaacgcat t

41

<210> 34
 <211> 41
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Double
 stranded oligonucleotide wherein n at position 10
 is a C/A mismatched base pair.

<220>
 <221> misc_feature
 <222> (10)

<223> The n at position 10 represents a C/A mismatched base pair.

<400> 34

cggtacaagn ccgtcacgaa ttaagcaatt cgtaacgcat t

41

<210> 35

<211> 41

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Double stranded oligonucleotide wherein n at position 5 is a C/A mismatched base pair.

<220>

<221> misc_feature

<222> (5)

<223> The n at position 5 represents a C/A mismatched base pair.

<400> 35

cggttcaagt ccgtcacgaa ttaagcaatt cgtaacgcat t

41

<210> 36

<211> 656

<212> PRT

<213> Neurospora crassa

<400> 36

Met Pro Ser Arg Lys Ser Lys Ala Ala Ala Leu Asp Thr Pro Gln Ser
1 5 10 15

Glu Ser Ser Thr Phe Ser Ser Thr Leu Asp Ser Ser Ala Pro Ser Pro
20 25 30

Ala Arg Asn Leu Arg Arg Ser Gly Arg Asn Ile Leu Gln Pro Ser Ser
35 40 45

Glu Lys Asp Arg Asp His Glu Lys Arg Ser Gly Glu Glu Leu Ala Gly
50 55 60

Arg Met Met Gly Lys Asp Ala Asn Gly His Cys Leu Arg Glu Gly Lys
65 70 75 80

Glu Gln Glu Glu Gly Val Lys Met Ala Ile Glu Gly Leu Ala Arg Met
85 90 95

Glu Arg Arg Leu Gln Arg Ala Thr Lys Arg Gln Lys Lys Gln Leu Glu
100 105 110

Glu	Asp	Gly	Ile	Pro	Val	Pro	Ser	Val	Val	Ser	Arg	Phe	Pro	Thr	Ala	
	115						120					125				
Pro	Tyr	His	His	Lys	Ser	Thr	Asn	Ala	Glu	Glu	Arg	Glu	Ala	Lys	Glu	
	130					135					140					
Pro	Val	Leu	Lys	Thr	His	Ser	Lys	Asp	Val	Glu	Arg	Glu	Ala	Glu	Ile	
145					150					155					160	
Gly	Val	Asp	Asp	Val	Val	Lys	Met	Glu	Pro	Ala	Ala	Thr	Asn	Ile	Ile	
				165					170					175		
Glu	Pro	Glu	Asp	Ala	Gln	Asp	Ala	Ala	Glu	Arg	Gly	Ala	Ala	Arg	Pro	
			180					185						190		
Pro	Ala	Val	Asn	Ser	Ser	Tyr	Leu	Pro	Leu	Pro	Trp	Lys	Gly	Arg	Leu	
	195						200					205				
Gly	Tyr	Ala	Cys	Leu	Asn	Thr	Tyr	Leu	Arg	Asn	Ala	Lys	Pro	Pro	Ile	
	210					215					220					
Phe	Ser	Ser	Arg	Thr	Cys	Arg	Met	Ala	Ser	Ile	Val	Asp	His	Arg	His	
225					230					235					240	
Pro	Leu	Gln	Phe	Glu	Asp	Glu	Pro	Glu	His	His	Leu	Lys	Asn	Lys	Pro	
				245					250					255		
Asp	Lys	Ser	Lys	Glu	Pro	Gln	Asp	Glu	Leu	Gly	His	Lys	Phe	Val	Gln	
			260					265					270			
Glu	Leu	Gly	Leu	Ala	Asn	Ala	Arg	Asp	Ile	Val	Lys	Met	Leu	Cys	Trp	
	275						280					285				
Asn	Glu	Lys	Tyr	Gly	Ile	Arg	Phe	Leu	Arg	Leu	Ser	Ser	Glu	Met	Phe	
	290					295					300					
Pro	Phe	Ala	Ser	His	Pro	Val	His	Gly	Tyr	Lys	Leu	Ala	Pro	Phe	Ala	
305					310					315					320	
Ser	Glu	Val	Leu	Ala	Glu	Ala	Gly	Arg	Val	Ala	Ala	Glu	Leu	Gly	His	
				325					330					335		
Arg	Leu	Thr	Thr	His	Pro	Gly	Gln	Phe	Thr	Gln	Leu	Gly	Ser	Pro	Arg	
			340					345					350			
Lys	Glu	Val	Val	Glu	Ser	Ala	Ile	Arg	Asp	Leu	Glu	Tyr	His	Asp	Glu	
	355						360					365				
Leu	Leu	Ser	Leu	Leu	Lys	Leu	Pro	Glu	Gln	Gln	Asn	Arg	Asp	Ala	Val	
	370					375					380					

104250-964260

Met	Ile	Ile	His	Met	Gly	Gly	Gln	Phe	Gly	Asp	Lys	Ala	Ala	Thr	Leu	385	390	395	400
Glu	Arg	Phe	Lys	Arg	Asn	Tyr	Ala	Arg	Leu	Ser	Gln	Ser	Cys	Lys	Asn	405	410	415	
Arg	Leu	Val	Leu	Glu	Asn	Asp	Asp	Val	Gly	Trp	Thr	Val	His	Asp	Leu	420	425	430	
Leu	Pro	Val	Cys	Glu	Glu	Leu	Asn	Ile	Pro	Met	Val	Leu	Asp	Tyr	His	435	440	445	
His	His	Asn	Ile	Cys	Phe	Asp	Pro	Ala	His	Leu	Arg	Glu	Gly	Thr	Leu	450	455	460	
Asp	Ile	Ser	Asp	Pro	Lys	Leu	Gln	Glu	Arg	Ile	Ala	Asn	Thr	Trp	Lys	465	470	475	480
Arg	Lys	Gly	Ile	Lys	Gln	Lys	Met	His	Tyr	Ser	Glu	Pro	Cys	Asp	Gly	485	490	495	
Ala	Val	Thr	Pro	Arg	Asp	Arg	Arg	Lys	His	Arg	Pro	Arg	Val	Met	Thr	500	505	510	
Leu	Pro	Pro	Cys	Pro	Pro	Asp	Met	Asp	Leu	Met	Ile	Glu	Ala	Lys	Asp	515	520	525	
Lys	Glu	Gln	Ala	Val	Phe	Glu	Leu	Met	Arg	Thr	Phe	Lys	Leu	Pro	Gly	530	535	540	
Phe	Glu	Lys	Ile	Asn	Asp	Met	Val	Pro	Tyr	Asp	Arg	Asp	Asp	Glu	Asn	545	550	555	560
Arg	Pro	Ala	Pro	Pro	Val	Lys	Ala	Pro	Lys	Lys	Lys	Lys	Gly	Gly	Lys	565	570	575	
Arg	Lys	Arg	Thr	Thr	Asp	Glu	Glu	Ala	Ala	Glu	Pro	Glu	Glu	Val	Asp	580	585	590	
Thr	Ala	Ala	Asp	Asp	Val	Lys	Asp	Ala	Pro	Glu	Gly	Pro	Lys	Glu	Val	595	600	605	
Pro	Glu	Glu	Glu	Arg	Ala	Met	Gly	Gly	Pro	Tyr	Asn	Arg	Val	Tyr	Trp	610	615	620	
Pro	Leu	Gly	Cys	Glu	Glu	Trp	Leu	Lys	Pro	Lys	Lys	Arg	Glu	Val	Lys	625	630	635	640
Lys	Gly	Lys	Val	Pro	Glu	Glu	Val	Glu	Asp	Glu	Gly	Glu	Phe	Asp	Gly	645	650	655	

<210> 37
 <211> 317
 <212> PRT
 <213> Bacillus subtilis

<400> 37

Met	Ile	Phe	Arg	Phe	Gly	Phe	Val	Ser	Asn	Ala	Met	Ser	Leu	Trp	Asp
1				5					10					15	
Ala	Ser	Pro	Ala	Lys	Thr	Leu	Thr	Phe	Ala	Arg	Tyr	Ser	Lys	Leu	Ser
			20					25					30		
Lys	Thr	Glu	Arg	Lys	Glu	Ala	Leu	Leu	Thr	Val	Thr	Lys	Ala	Asn	Leu
		35					40					45			
Arg	Asn	Thr	Met	Arg	Thr	Leu	His	Tyr	Ile	Ile	Gly	His	Gly	Ile	Pro
	50					55					60				
Leu	Tyr	Arg	Phe	Ser	Ser	Ser	Ile	Val	Pro	Leu	Ala	Thr	His	Pro	Asp
65					70					75					80
Val	Met	Trp	Asp	Phe	Val	Thr	Pro	Phe	Gln	Lys	Glu	Phe	Arg	Glu	Ile
				85					90					95	
Gly	Glu	Leu	Val	Lys	Thr	His	Gln	Leu	Arg	Thr	Ser	Phe	His	Pro	Asn
		100						105					110		
Gln	Phe	Thr	Leu	Phe	Thr	Ser	Pro	Lys	Glu	Ser	Val	Thr	Lys	Asn	Ala
	115						120					125			
Val	Thr	Asp	Met	Ala	Tyr	His	Tyr	Arg	Met	Leu	Glu	Ala	Met	Gly	Ile
	130					135					140				
Ala	Asp	Arg	Ser	Val	Ile	Asn	Ile	His	Ile	Gly	Gly	Ala	Tyr	Gly	Asn
145					150					155					160
Lys	Asp	Thr	Ala	Thr	Ala	Gln	Phe	His	Gln	Asn	Ile	Lys	Gln	Leu	Pro
			165						170					175	
Gln	Glu	Ile	Lys	Glu	Arg	Met	Thr	Leu	Glu	Asn	Asp	Asp	Lys	Thr	Tyr
		180						185					190		
Thr	Thr	Glu	Glu	Thr	Leu	Gln	Val	Cys	Glu	Gln	Glu	Asp	Val	Pro	Phe
	195						200					205			
Val	Phe	Asp	Phe	His	His	Phe	Tyr	Ala	Asn	Pro	Asp	Asp	His	Ala	Asp
	210					215						220			

Leu Asn Val Ala Leu Pro Arg Met Ile Lys Thr Trp Glu Arg Ile Gly
 225 230 235 240
 Leu Gln Pro Lys Val His Leu Ser Ser Pro Lys Ser Glu Gln Ala Ile
 245 250 255
 Arg Ser His Ala Asp Tyr Val Asp Ala Asn Phe Leu Leu Glu Arg Phe
 260 265 270
 Arg Gln Trp Gly Thr Asn Ile Asp Phe Met Ile Glu Ala Lys Gln Lys
 275 280 285
 Asp Lys Ala Leu Leu Arg Leu Met Asp Glu Leu Ser Ser Ile Arg Gly
 290 295 300
 Val Lys Arg Ile Gly Gly Gly Ala Leu Gln Trp Lys Ser
 305 310 315

<210> 38
 <211> 580
 <212> PRT
 <213> Homo sapiens

<400> 38
 Met Gly Thr Thr Gly Leu Glu Ser Leu Ser Leu Gly Asp Arg Gly Ala
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 Ala Pro Thr Val Thr Ser Ser Glu Arg Leu Val Pro Asp Pro Pro Asn
 20 25 30
 Asp Leu Arg Lys Glu Asp Val Ala Met Glu Leu Glu Arg Val Gly Glu
 35 40 45
 Asp Glu Glu Gln Met Met Ile Lys Arg Ser Ser Glu Cys Asn Pro Leu
 50 55 60
 Leu Gln Glu Pro Ile Ala Ser Ala Gln Phe Gly Ala Thr Ala Gly Thr
 65 70 75 80
 Glu Cys Arg Lys Ser Val Pro Cys Gly Trp Glu Arg Val Val Lys Gln
 85 90 95
 Arg Leu Phe Gly Lys Thr Ala Gly Arg Phe Asp Val Tyr Phe Ile Ser
 100 105 110
 Pro Gln Gly Leu Lys Phe Arg Ser Lys Ser Ser Leu Ala Asn Tyr Leu
 115 120 125
 His Lys Asn Gly Glu Thr Ser Leu Lys Pro Glu Asp Phe Asp Phe Thr
 130 135 140

Val	Leu	Ser	Lys	Arg	Gly	Ile	Lys	Ser	Arg	Tyr	Lys	Asp	Cys	Ser	Met		
145					150					155					160		
Ala	Ala	Leu	Thr	Ser	His	Leu	Gln	Asn	Gln	Ser	Asn	Asn	Ser	Asn	Trp		
				165					170						175		
Asn	Leu	Arg	Thr	Arg	Ser	Lys	Cys	Lys	Lys	Asp	Val	Phe	Met	Pro	Pro		
			180					185					190				
Ser	Ser	Ser	Ser	Glu	Leu	Gln	Glu	Ser	Arg	Gly	Leu	Ser	Asn	Phe	Thr		
			195				200					205					
Ser	Thr	His	Leu	Leu	Leu	Lys	Glu	Asp	Glu	Gly	Val	Asp	Asp	Val	Asn		
	210					215					220						
Phe	Arg	Lys	Val	Arg	Lys	Pro	Lys	Gly	Lys	Val	Thr	Ile	Leu	Lys	Gly		
225					230					235					240		
Ile	Pro	Ile	Lys	Lys	Thr	Lys	Lys	Gly	Cys	Arg	Lys	Ser	Cys	Ser	Gly		
			245					250						255			
Phe	Val	Gln	Ser	Asp	Ser	Lys	Arg	Glu	Ser	Val	Cys	Asn	Lys	Ala	Asp		
			260					265					270				
Ala	Glu	Ser	Glu	Pro	Val	Ala	Gln	Lys	Ser	Gln	Leu	Asp	Arg	Thr	Val		
	275						280					285					
Cys	Ile	Ser	Asp	Ala	Gly	Ala	Cys	Gly	Glu	Thr	Leu	Ser	Val	Thr	Ser		
	290					295					300						
Glu	Glu	Asn	Ser	Leu	Val	Lys	Lys	Lys	Glu	Arg	Ser	Leu	Ser	Ser	Gly		
305				310					315						320		
Ser	Asn	Phe	Cys	Ser	Glu	Gln	Lys	Thr	Ser	Gly	Ile	Ile	Asn	Lys	Phe		
			325					330						335			
Cys	Ser	Ala	Lys	Asp	Ser	Glu	His	Asn	Glu	Lys	Tyr	Glu	Asp	Thr	Phe		
		340						345					350				
Leu	Glu	Ser	Glu	Glu	Ile	Gly	Thr	Lys	Val	Glu	Val	Val	Glu	Arg	Lys		
	355						360					365					
Glu	His	Leu	His	Thr	Asp	Ile	Leu	Lys	Arg	Gly	Ser	Glu	Met	Asp	Asn		
	370					375					380						
Asn	Cys	Ser	Pro	Thr	Arg	Lys	Asp	Phe	Thr	Gly	Glu	Lys	Ile	Phe	Gln		
385					390					395					400		
Glu	Asp	Thr	Ile	Pro	Arg	Thr	Gln	Ile	Glu	Arg	Arg	Lys	Thr	Ser	Leu		
			405						410					415			

Tyr Phe Ser Ser Lys Tyr Asn Lys Glu Ala Leu Ser Pro Pro Arg Arg
 420 425 430

Lys Ala Phe Lys Lys Trp Thr Pro Pro Arg Ser Pro Phe Asn Leu Val
 435 440 445

Gln Glu Thr Leu Phe His Asp Pro Trp Lys Leu Leu Ile Ala Thr Ile
 450 455 460

Phe Leu Asn Arg Thr Ser Gly Lys Met Ala Ile Pro Val Leu Trp Lys
 465 470 475 480

Phe Leu Glu Lys Tyr Pro Ser Ala Glu Val Ala Arg Thr Ala Asp Trp
 485 490 495

Arg Asp Val Ser Glu Leu Leu Lys Pro Leu Gly Leu Tyr Asp Leu Arg
 500 505 510

Ala Lys Thr Ile Val Lys Phe Ser Asp Glu Tyr Leu Thr Lys Gln Trp
 515 520 525

Lys Tyr Pro Ile Glu Leu His Gly Ile Gly Lys Tyr Gly Asn Asp Ser
 530 535 540

Tyr Arg Ile Phe Cys Val Asn Glu Trp Lys Gln Val His Pro Glu Asp
 545 550 555 560

His Lys Leu Asn Lys Tyr His Asp Trp Leu Trp Glu Asn His Glu Lys
 565 570 575

Leu Ser Leu Ser
 580

<210> 39

<211> 294

<212> PRT

<213> Deinococcus radiodurans

<400> 39

Gln Leu Gly Leu Val Cys Leu Thr Val Gly Pro Glu Val Arg Phe Arg
 1 5 10 15

Thr Val Thr Leu Ser Arg Tyr Arg Ala Leu Ser Pro Ala Glu Arg Glu
 20 25 30

Ala Lys Leu Leu Asp Leu Tyr Ser Ser Asn Ile Lys Thr Leu Arg Gly
 35 40 45

Ala Ala Asp Tyr Cys Ala Ala His Asp Ile Arg Leu Tyr Arg Leu Ser
 50 55 60

Ser Ser Leu Phe Pro Met Leu Asp Leu Ala Gly Asp Asp Thr Gly Ala
 65 70 75 80
 Ala Val Leu Thr His Leu Ala Pro Gln Leu Leu Glu Ala Gly His Ala
 85 90 95
 Phe Thr Asp Ala Gly Val Arg Leu Leu Met His Pro Glu Gln Phe Ile
 100 105 110
 Val Leu Asn Ser Asp Arg Pro Glu Val Arg Glu Ser Ser Val Arg Ala
 115 120 125
 Met Ser Ala His Ala Arg Val Met Asp Gly Leu Gly Leu Ala Arg Thr
 130 135 140
 Pro Trp Asn Leu Leu Leu Leu His Gly Gly Lys Gly Gly Arg Gly Ala
 145 150 155 160
 Glu Leu Ala Ala Leu Ile Pro Asp Leu Pro Asp Pro Val Arg Leu Arg
 165 170 175
 Leu Gly Leu Glu Asn Asp Glu Arg Ala Tyr Ser Pro Ala Glu Leu Leu
 180 185 190
 Pro Ile Cys Glu Ala Thr Gly Thr Pro Leu Val Phe Asp Ala His His
 195 200 205
 His Val Val His Asp Lys Leu Pro Asp Gln Glu Asp Pro Ser Val Arg
 210 215 220
 Glu Trp Val Leu Arg Ala Arg Ala Thr Trp Gln Pro Pro Glu Trp Gln
 225 230 235 240
 Val Val His Leu Ser Asn Gly Ile Glu Gly Pro Gln Asp Arg Arg His
 245 250 255
 Ser His Leu Ile Ala Asp Phe Pro Ser Ala Tyr Ala Asp Val Pro Gln
 260 265 270
 Ile Glu Val Glu Ala Lys Gly Lys Glu Glu Ala Ile Ala Ala Leu Arg
 275 280 285
 Leu Met Ala Pro Phe Lys
 290

<210> 40

<211> 39

<212> DNA

<213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:
 Oligonucleotide

<400> 40
 cacagactcc ctctgtcata ggtttgagtt tatatggaa 39

<210> 41
 <211> 39
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:
 Oligonucleotide

<400> 41
 ttccatataa actcaaacct atgacagagg gagtctgtg 39

<210> 42
 <211> 41
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:
 Oligonucleotide

<400> 42
 cacagactcc ctctgtcata ggttcatgag tttatatgga a 41

<210> 43
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 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:
 Oligonucleotide

<400> 43
 cacagactcc ctctgtcata ggttcacatg agtttatatg gaa 43

<210> 44
 <211> 45
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:
 Oligonucleotide

<400> 44
cacagactcc ctctgtcata ggttcacaca tgagtttata tggaa 45

<210> 45
<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide

<400> 45
cacagactcc ctctgtcata ggttcacaca catgagttta tatggaa 47

<210> 46
<211> 53
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide

<400> 46
cacagactcc ctctgtcata ggttgagtac tagtactctg agtttatatg gaa 53

<210> 47
<211> 41
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide

<400> 47
cgttagaact ccgtcacgaa ttaagcaatt agtaatgcat t 41

<210> 48
<211> 41
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide

<400> 48
aatgcattac taattgctta attcgtgacg gagttctaac g 41

<210> 49
<211> 43
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide

<400> 49
cgttagaact ccgtcacgaa ttaagcaatt caagtaatgc att 43

<210> 50
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide

<400> 50
cgttagaact ccgtcacgaa ttaagcaatt cacaagtaat gcatt 45

<210> 51
<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide

<400> 51
cgttagaact ccgtcacgaa ttaagcaatt cacacaagta atgcatt 47

<210> 52
<211> 49
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide

<400> 52
cgttagaact ccgtcacgaa ttaagcaatt cacacacaag taatgcatt 49

<210> 53
<211> 41
<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
Oligonucleotide

<400> 53

cgttacaagt ccgtcacgaa ttaagcaatt cgtaacgcat t 41

<210> 54

<211> 41

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:
Oligonucleotide

<400> 54

aatgcattac gaattgctta attcgtgacg gacttgtaac g 41

<210> 55

<211> 41

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:
Oligonucleotide

<400> 55

cgttacaagt ccgtcacgaa ttaagcaatt cgtaacgcat t 41

<210> 56

<211> 41

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:
Oligonucleotide

<400> 56

aatgcgttac aaattgctta attcgtgacg gacttgtaac g 41

<210> 57

<211> 41

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:
Oligonucleotide

<400> 57

cgttacaagt ccgtcacgaa ttaagcaatt cgtaacgcat t 41

<210> 58

<211> 41

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
Oligonucleotide

<400> 58

aatgcgttac gaattactta attcgtgacg gacttgtaac g 41

<210> 59

<211> 41

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
Oligonucleotide

<400> 59

cgttacaagt ccgtcacgac ttaagcaatt cgtaacgcat t 41

<210> 60

<211> 41

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
Oligonucleotide

<400> 60

aatgcgttac gaattgctta aatcgtgacg gacttgtaac g 41

<210> 61

<211> 41

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
Oligonucleotide

09744296-052704

<400> 61
cggtacaagt ccgtcacgaa ttaagcaatt cgtaacgcat t 41

<210> 62
<211> 41
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<223> Description of Artificial Sequence:
Oligonucleotide

<400> 62
aatgcgttac gaattgctta attcgtaacg gacttgtaac g 41

<210> 63
<211> 41
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide

<400> 63
cgttacaagc ccgtcacgaa ttaagcaatt cgtaacgcat t 41

<210> 64
<211> 41
<212> DNA
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<220>
<223> Description of Artificial Sequence:
Oligonucleotide

<400> 64
aatgcgttac gaattgctta attcgtgacg gacttgtaac g 41

<210> 65
<211> 41
<212> DNA
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<220>
<223> Description of Artificial Sequence:
Oligonucleotide

<400> 65
cgttccaagt ccgtcacgaa ttaagcaatt cgtaacgcat t 41

<210> 66
<211> 41
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide

<400> 66
aatgcgttac gaattgctta attcgtgacg gacttgaaac g 41

<210> 67
<211> 78
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide

<400> 67
tgcacggacc tcgagagaac cgaacgatcc ggatgtgac atgggacaga attcgcacac 60
tgcaactcgac gatagtct 78

<210> 68
<211> 49
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide

<400> 68
tgcagtgtgc gaattctgtc ccatcatcac atccggatcg ttcggttct 49

<210> 69
<211> 62
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide

<400> 69
gactatcgtg cagtgcagtg tgcgaattct gtcccatcat cacatccgga tcgttcggtt 60
ct 62

<210> 70

<211> 64
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide

<400> 70
tgcagtgtgc gaattctgtc ccatcatcac atccggatcg ttcggttctc tcgaggtccg 60
tgca 64

<210> 71
<211> 79
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide

<400> 71
gagactatcg tgcagtgcag tgtgcgaatt ctgtcccatc atcacatccg gatcgttcgg 60
ttctctcgag gtccgtgca 79